

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| M | C | P | S | Q | P | T | Y | P | G | D | P | G | P |
| ATG | TGC | CCG | AGC | CAG | CCG | ACC | TAT | CCG | GGC | GAT | CCC | GGG | CCG |
| | | | | | | | | | | | | | |
| V | E | D | L | I | R | F | Y | D | N | L | Q | Q | W |
| GTG | GAA | GAT | CTG | ATC | CGC | TTT | TAT | GAT | AAC | CTG | CAG | CAG | TGG |
| | | | | | | | | | | | | | |
| L | N | C | V | T | A | A | C | * | | | | | |
| CTG | AAC | TGC | GTG | ACC | GCC | GCC | TGC | TAG | | | | | |

FIGURE 1

10027038-122001

| | | | | |
|------------|-------------|------------|------------|------------|
| 1 | 11 | 21 | 31 | 41 |
| ACACACCATA | TGTGCCCCGAG | CCAGCCGACC | TATCCGGGCG | ATCCCGGGCC |
| TGTGTGGTAT | ACACGGGCTC | GGTCGGCTGG | ATAGGCCCGC | TAGGGCCCCG |

| | | | | |
|------------|------------|------------|------------|------------|
| 51 | 61 | 71 | 81 | 91 |
| GGTGGAAGAT | CTGATCCGCT | TTTATGATAA | CCTGCAGCAG | TGGCTGAACT |
| CCACCTTCTA | GACTAGGCGA | AAATACTATT | GGACGTCGTC | ACCGACTTGA |

| | | | |
|------------|------------|------------|-----|
| 101 | 111 | 121 | 131 |
| GCGTGACCGC | CGCCTGCTAG | GGATCCACAC | AC |
| CGCACTGGCG | GCGGACGATC | CCTAGGTGTG | TG |

FIGURE 2

10027038.122004

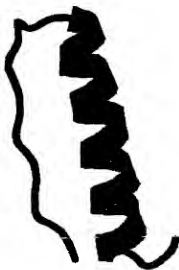


FIGURE 3

10027038.122001

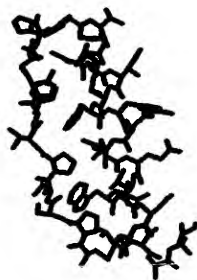


FIGURE 4

10027030.122001



FIGURE 5

10027038.122001

10027038.12001

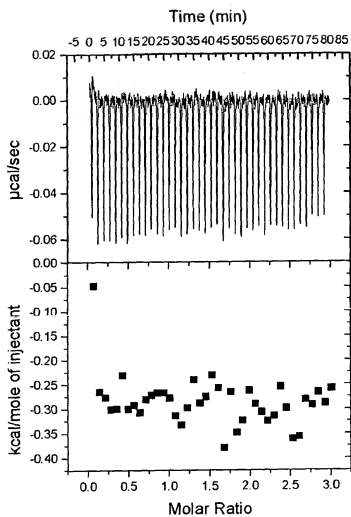


FIGURE 6

10027038.122001

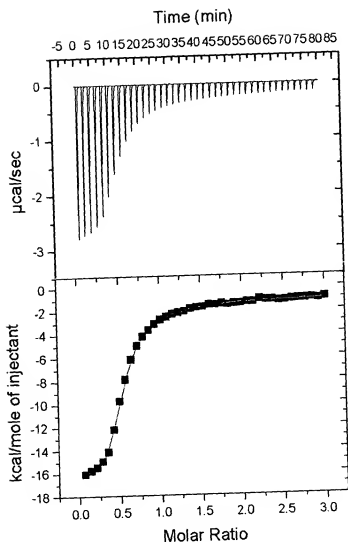


FIGURE 7

10027038, 122001

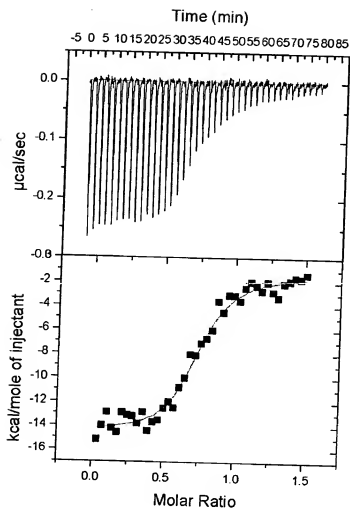


FIGURE 8

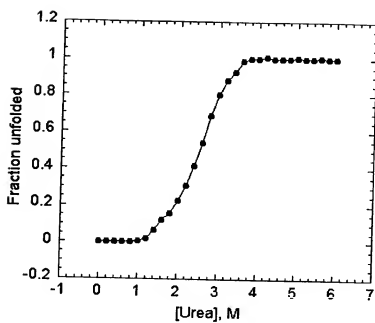


FIGURE 9

10027038-122001

10027038-122004

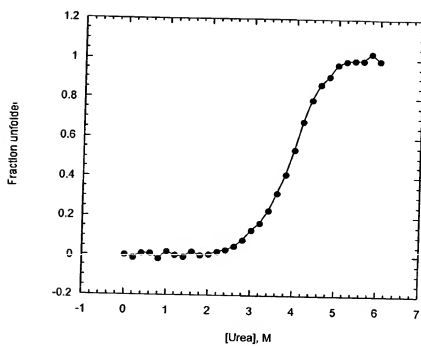


FIGURE 10

10027038-122001

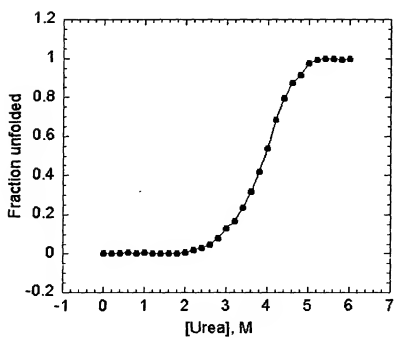


FIGURE 11

10027036-122001

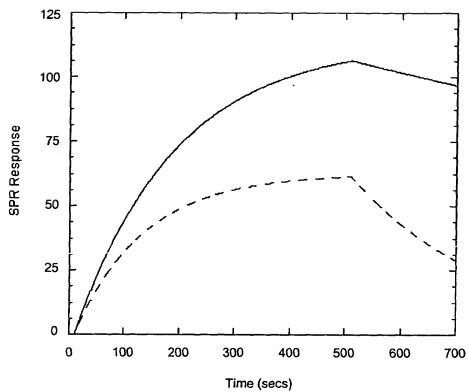


FIGURE 12

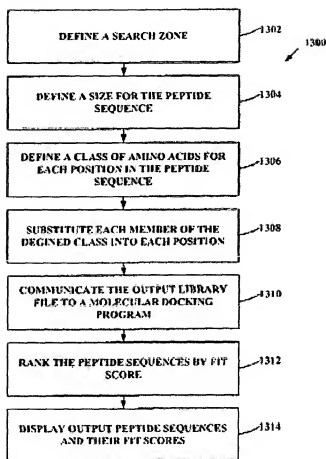


FIG. 13

1002030.12001

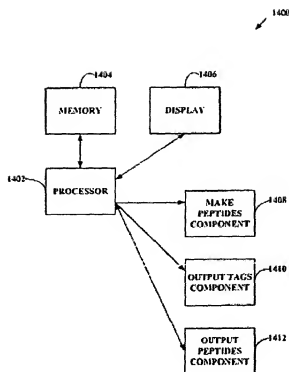


FIG. 14

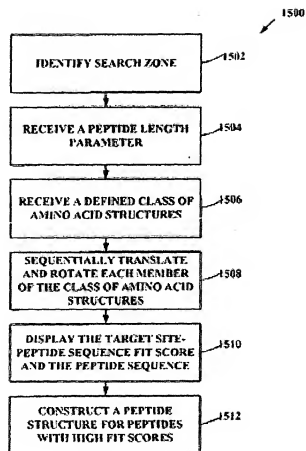


FIG. 15